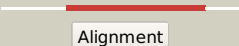
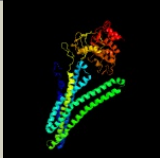

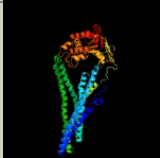
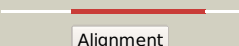





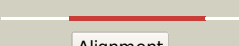
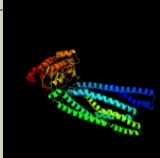

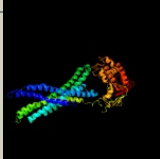

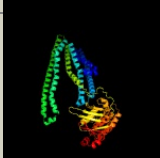

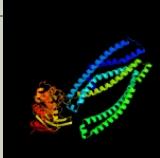



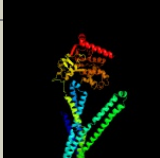
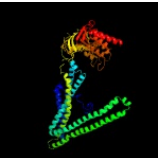




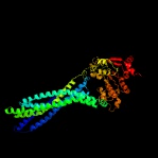





Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1348 (-) _1513053_1515632 |
| Date | Wed Jul 31 22:05:45 BST 2019 |
| Unique Job ID | 0791d73fda7a0641 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c4ry2A_ |  Alignment |  | 100.0 | 26 | PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1 |
| 2 | c3qf4A_ |  Alignment |  | 100.0 | 26 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation |
| 3 | c5mkkA_ |  Alignment |  | 100.0 | 29 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap |
| 4 | c5mkkB_ |  Alignment |  | 100.0 | 26 | PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap |
| 5 | c3qf4B_ |  Alignment |  | 100.0 | 27 | PDB header: transport protein Chain: B: PDB Molecule: uncharacterized abc transporter atp-binding protein PDBTitle: crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation |
| 6 | c5ochF_ |  Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: F: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state |
| 7 | c2hydB_ |  Alignment |  | 100.0 | 25 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866 |
| 8 | c3wmeA_ |  Alignment |  | 100.0 | 26 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette, sub-family b, member 1; PDBTitle: crystal structure of an inward-facing eukaryotic abc multidrug2 transporter |
| 9 | c2yl4A_ |  Alignment |  | 100.0 | 29 | PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10 |
| 10 | c5u1dA_ |  Alignment |  | 100.0 | 26 | PDB header: transport protein Chain: A: PDB Molecule: antigen peptide transporter 1; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter |
| 11 | c4mycC_ |  Alignment |  | 100.0 | 24 | PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial; PDBTitle: structure of the mitochondrial abc transporter, atm1 |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c4f4cA_ | Alignment |  | 100.0 | 23 | PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter |
| 13 | c4mrnB_ | Alignment |  | 100.0 | 26 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter |
| 14 | c4aa3A_ | Alignment |  | 100.0 | 29 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter,2 abcb10 (plate form) |
| 15 | c6bhuA_ | Alignment |  | 100.0 | 20 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: cryo-em structure of atp-bound, outward-facing bovine multidrug2 resistance protein 1 (mrp1) |
| 16 | c4pl0B_ | Alignment |  | 100.0 | 18 | PDB header: transport protein Chain: B: PDB Molecule: microcin-j25 export atp-binding/permease protein mcjd; PDBTitle: crystal structure of the antibacterial peptide abc transporter mcjd in2 an outward occluded state |
| 17 | c6c0vA_ | Alignment |  | 100.0 | 25 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance protein 1; PDBTitle: molecular structure of human p-glycoprotein in the atp-bound, outward-2 facing conformation |
| 18 | c5ochH_ | Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: H: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state |
| 19 | c6c3oE_ | Alignment |  | 100.0 | 22 | PDB header: transport protein Chain: E: PDB Molecule: atp-binding cassette sub-family c member 8; PDBTitle: cryo-em structure of human katp bound to atp and adp in quatrefoil2 form |
| 20 | c5ykhH_ | Alignment |  | 100.0 | 22 | PDB header: membrane protein Chain: H: PDB Molecule: atp-binding cassette sub-family c member 8 isoform x2; PDBTitle: structure of pancreatic atp-sensitive potassium channel bound with2 glibenclamide and atpgammas (3d class1 at 4.33a) |
| 21 | c3g5uB_ | Alignment | not modelled | 100.0 | 25 | PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding |
| 22 | c5ujaA_ | Alignment | not modelled | 100.0 | 21 | PDB header: protein transport Chain: A: PDB Molecule: bovine multidrug resistance protein 1 (mrp1),multidrug PDBTitle: cryo-em structure of bovine multidrug resistance protein 1 (mrp1)2 bound to leukotriene c4 |
| 23 | c5uj9A_ | Alignment | not modelled | 100.0 | 21 | PDB header: transport protein Chain: A: PDB Molecule: bovine multidrug resistance protein 1 (mrp1),multidrug PDBTitle: cryo-em structure of bovine multidrug resistance protein 1 (mrp1) |
| 24 | c3b5wE_ | Alignment | not modelled | 100.0 | 28 | PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba |
| 25 | c5u1dB_ | Alignment | not modelled | 100.0 | 26 | PDB header: transport protein Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter |
| 26 | c5wuaF_ | Alignment | not modelled | 100.0 | 23 | PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel |
| 27 | c5j22B_ | Alignment | not modelled | 100.0 | 22 | PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prttd t1ss abc transporter |
| 28 | c5u71A_ | Alignment | not modelled | 100.0 | 18 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| | | | | | | PDBTitle: structure of human cystic fibrosis transmembrane conductance regulator2 (cftr) |
| 29 | c5tsiA_ | Alignment | not modelled | 100.0 | 16 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of the cystic fibrosis transmembrane conductance regulator2 (cftr) from zebrafish |
| 30 | c3b5xB_ | Alignment | not modelled | 100.0 | 29 | PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae |
| 31 | c5c76D_ | Alignment | not modelled | 100.0 | 20 | PDB header: transport protein Chain: D: PDB Molecule: wlab protein; PDBTitle: atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2) |
| 32 | c3nhaA_ | Alignment | not modelled | 100.0 | 40 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 6, mitochondrial; PDBTitle: nucleotide binding domain of human abcb6 (adp mg bound structure) |
| 33 | c5idvA_ | Alignment | not modelled | 100.0 | 47 | PDB header: transport protein Chain: A: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: structure of the nucleotide binding domain of an abc transporter msba2 from acinetobacter baumannii |
| 34 | c3vx4D_ | Alignment | not modelled | 100.0 | 35 | PDB header: transport protein Chain: D: PDB Molecule: putative abc transporter, atp-binding protein coma; PDBTitle: crystal structure of the nucleotide-binding domain of s. mutans coma,2 a bifunctional atp-binding cassette transporter involved in the3 quorum-sensing pathway |
| 35 | d2pmka1 | Alignment | not modelled | 100.0 | 39 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 36 | d2hyda1 | Alignment | not modelled | 100.0 | 44 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 37 | d3b60a1 | Alignment | not modelled | 100.0 | 46 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 38 | c6bzaA_ | Alignment | not modelled | 100.0 | 34 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state |
| 39 | d1jj7a_ | Alignment | not modelled | 100.0 | 38 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 40 | d1mv5a_ | Alignment | not modelled | 100.0 | 39 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 41 | c6bzsa_ | Alignment | not modelled | 100.0 | 29 | PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state |
| 42 | c2cbzA_ | Alignment | not modelled | 100.0 | 24 | PDB header: transport Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: structure of the human multidrug resistance protein 12 nucleotide binding domain 1 |
| 43 | c5dgaA_ | Alignment | not modelled | 100.0 | 40 | PDB header: transport protein Chain: A: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: 1.73 angstrom resolution crystal structure of the abc-atpase domain2 (residues 357-609) of lipid a transport protein (msba) from3 francisella tularensis subsp. tularensis schu s4 in complex with adp |
| 44 | c2ghiD_ | Alignment | not modelled | 100.0 | 38 | PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance protein 2 |
| 45 | c2iw3B_ | Alignment | not modelled | 100.0 | 15 | PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp |
| 46 | c2r6fA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra |
| 47 | c5x7kB_ | Alignment | not modelled | 100.0 | 38 | PDB header: transport protein Chain: B: PDB Molecule: lipase b; PDBTitle: crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system |
| 48 | c5x5yB_ | Alignment | not modelled | 100.0 | 24 | PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex |
| 49 | c2olkD_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s |
| 50 | c1z47B_ | Alignment | not modelled | 100.0 | 27 | PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius |
| 51 | c4huqB_ | Alignment | not modelled | 100.0 | 28 | PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfa PDBTitle: crystal structure of a transporter |
| 52 | c5vivA_ | Alignment | not modelled | 100.0 | 25 | PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 52 | c2xyA_ | Alignment | not modelled | 100.0 | 25 | 1; PDBTitle: cryo-em structure of human abca1 |
| 53 | c2pzfB_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: B; PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508 |
| 54 | d1pf4a1 | Alignment | not modelled | 100.0 | 44 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 55 | c3gfoA_ | Alignment | not modelled | 100.0 | 23 | PDB header: atp binding protein Chain: A; PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq. |
| 56 | c5x40A_ | Alignment | not modelled | 100.0 | 26 | PDB header: transport protein Chain: A; PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp |
| 57 | c3gd7C_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: C; PDB Molecule: fusion complex of cystic fibrosis transmembrane conductance PDBTitle: crystal structure of human nbd2 complexed with n6-phenylethyl-atp (p-2 atp) |
| 58 | c5ws4A_ | Alignment | not modelled | 100.0 | 28 | PDB header: membrane protein Chain: A; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii |
| 59 | c4hluC_ | Alignment | not modelled | 100.0 | 29 | PDB header: hydrolase Chain: C; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp |
| 60 | c4tqvO_ | Alignment | not modelled | 100.0 | 33 | PDB header: transport protein Chain: O; PDB Molecule: algs; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate |
| 61 | c5d3mF_ | Alignment | not modelled | 100.0 | 24 | PDB header: transport protein Chain: F; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state |
| 62 | c4p31B_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: B; PDB Molecule: lipopolysaccharide export system atp-binding protein lptb; PDBTitle: crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium |
| 63 | c2yyzA_ | Alignment | not modelled | 100.0 | 30 | PDB header: transport protein Chain: A; PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein |
| 64 | d1ji0a_ | Alignment | not modelled | 100.0 | 23 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 65 | c5do7A_ | Alignment | not modelled | 100.0 | 27 | PDB header: transport protein Chain: A; PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8 |
| 66 | c4fwiB_ | Alignment | not modelled | 100.0 | 26 | PDB header: transport protein Chain: B; PDB Molecule: abc-type dipeptide/oligopeptide/nickel transport system, PDBTitle: crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter |
| 67 | d1r0wa_ | Alignment | not modelled | 100.0 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 68 | c2it1B_ | Alignment | not modelled | 100.0 | 29 | PDB header: transport protein Chain: B; PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii |
| 69 | c3fvqB_ | Alignment | not modelled | 100.0 | 29 | PDB header: hydrolase Chain: B; PDB Molecule: fe(3+) ions import atp-binding protein fbpc; PDBTitle: crystal structure of the nucleotide binding domain fbpc complexed with2 atp |
| 70 | c4ymuj_ | Alignment | not modelled | 100.0 | 31 | PDB header: protein binding/transport protein Chain: J; PDB Molecule: abc-type polar amino acid transport system, atpase PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps |
| 71 | c4mkiB_ | Alignment | not modelled | 100.0 | 27 | PDB header: hydrolase Chain: B; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit |
| 72 | c2d2fA_ | Alignment | not modelled | 100.0 | 27 | PDB header: protein binding Chain: A; PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufcd from thermus2 thermophilus hb8 |
| 73 | d1g6ha_ | Alignment | not modelled | 100.0 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 74 | c5lj7B_ | Alignment | not modelled | 100.0 | 30 | PDB header: transport protein Chain: B; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21) |
| 75 | c4wbsA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transport protein Chain: A; PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum |
| | | | | | | Fold: P-loop containing nucleoside triphosphate hydrolases |

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|-----|-------------------------|-----------|--------------|-------|----|--|
| 76 | d1xmia_ | Alignment | not modelled | 100.0 | 25 | Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 77 | d3dhwC1 | Alignment | not modelled | 100.0 | 29 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 78 | c1oxTB_ | Alignment | not modelled | 100.0 | 28 | PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus |
| 79 | c1vciA_ | Alignment | not modelled | 100.0 | 27 | PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp |
| 80 | c4u02C_ | Alignment | not modelled | 100.0 | 30 | PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159 |
| 81 | c3dhwC_ | Alignment | not modelled | 100.0 | 29 | PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni |
| 82 | d1vpla_ | Alignment | not modelled | 100.0 | 22 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 83 | c5d3mA_ | Alignment | not modelled | 100.0 | 31 | PDB header: transport protein Chain: A: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state |
| 84 | c2d62A_ | Alignment | not modelled | 100.0 | 27 | PDB header: sugar binding protein Chain: A: PDB Molecule: multiple sugar-binding transport atp-binding protein PDBTitle: crystal structure of multiple sugar binding transport atp-2 binding protein |
| 85 | d1v43a3 | Alignment | not modelled | 100.0 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 86 | d1b0ua_ | Alignment | not modelled | 100.0 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 87 | c4hzuB_ | Alignment | not modelled | 100.0 | 28 | PDB header: hydrolase, transport protein Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfA PDBTitle: structure of a bacterial energy-coupling factor transporter |
| 88 | d3d31a2 | Alignment | not modelled | 100.0 | 28 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 89 | c2yz2B_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system |
| 90 | d1g2912 | Alignment | not modelled | 100.0 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 91 | d1oxk2 | Alignment | not modelled | 100.0 | 25 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 92 | c6ic4I_ | Alignment | not modelled | 100.0 | 28 | PDB header: protein transport Chain: I: PDB Molecule: abc transporter atp-binding protein; PDBTitle: cryo-em structure of the a. baumannii mia complex at 8.7 a resolution |
| 93 | c5nikK_ | Alignment | not modelled | 100.0 | 33 | PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump |
| 94 | c4rvCA_ | Alignment | not modelled | 100.0 | 24 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter |
| 95 | d1l2ta_ | Alignment | not modelled | 100.0 | 26 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 96 | c1q1bD_ | Alignment | not modelled | 100.0 | 32 | PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form |
| 97 | c4g1uD_ | Alignment | not modelled | 100.0 | 29 | PDB header: transport protein/hydrolase Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis |
| 98 | c2pcjB_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein loid; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5 |
| 99 | c5do7B_ | Alignment | not modelled | 100.0 | 29 | PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8 |
| 100 | c4hziA_ | Alignment | not modelled | 100.0 | 23 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| 100 | c4n2IA | Alignment | not modelled | 100.0 | 29 | PDBTitle: crystal structure of the leptospira interrogans atpase subunit of an2 orphan abc transporter PDB header: transport protein |
| 101 | c3d31B | Alignment | not modelled | 100.0 | 29 | Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans |
| 102 | c5xu1A | Alignment | not modelled | 100.0 | 26 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6 |
| 103 | c5nj3B | Alignment | not modelled | 100.0 | 27 | PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure |
| 104 | c4yerB | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution |
| 105 | c2nq2C | Alignment | not modelled | 100.0 | 24 | PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter. |
| 106 | c6k2IA | Alignment | not modelled | 100.0 | 23 | PDB header: flavoprotein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of the siderophore-interacting protein sips from2 aeromonas hydrophila |
| 107 | c2gpiA | Alignment | not modelled | 100.0 | 26 | PDB header: fad-binding protein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution |
| 108 | d2onka1 | Alignment | not modelled | 100.0 | 29 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 109 | c2d3wB | Alignment | not modelled | 100.0 | 25 | PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcc; PDBTitle: crystal structure of escherichia coli sufcc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery |
| 110 | c6amxA | Alignment | not modelled | 100.0 | 23 | PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter |
| 111 | c5zxdB | Alignment | not modelled | 100.0 | 24 | PDB header: translation Chain: B: PDB Molecule: atp-binding cassette sub-family f member 1; PDBTitle: crystal structure of atp-bound human abcf1 |
| 112 | c2ygrD | Alignment | not modelled | 100.0 | 28 | PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra |
| 113 | c2ihyB | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter |
| 114 | c5b57D | Alignment | not modelled | 100.0 | 28 | PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: inward-facing conformation of abc heme importer bhuvv from2 burkholderia cenocepacia |
| 115 | c2pjzA | Alignment | not modelled | 100.0 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st1066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066 |
| 116 | c4yhbA | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: iron-chelator utilization protein; PDBTitle: crystal structure of a siderophore utilization protein from t. fusca |
| 117 | d1sgwa | Alignment | not modelled | 100.0 | 21 | Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like |
| 118 | c1yqtA | Alignment | not modelled | 100.0 | 27 | PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor |
| 119 | c4finA | Alignment | not modelled | 100.0 | 24 | PDB header: atp-binding protein Chain: A: PDB Molecule: etta (yjjk) abcf family protein; PDBTitle: crystal structure of etta (formerly yjjk) - an e. coli abc-type atpase |
| 120 | c6gehA | Alignment | not modelled | 100.0 | 24 | PDB header: metal transport Chain: A: PDB Molecule: fad-binding 9, siderophore-interacting domain protein; PDBTitle: structure and reactivity of a siderophore-interacting protein from the2 marine bacterium shewanella reveals unanticipated functional3 versatility. |